Fig.1A.

```
     M  V  N  R  S  V  A  F  S  A  F  V  L  I  L  F  V  L  A  I
1    ATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCGTTCTGATCCTTTTCGTGCTCGCCATC

     S
61   TCAGGTTATCAAATCTTTAGTTCATTTATTGAATATGATAGTATTTATATTCTTTTATGG
                                             intron
                                             D  I  A  S  V  S  G  E
121  TTTTATGTGTTCTGACAAGTTGCAAATATTGAGTAGATATCGCATCCGTTAGTGGAGAAC

     L  C  E  K  A  S  K  T  W  S  G  N  C  G  N  T  G  H  C  D
181  TATGCGAGAAAGCTAGCAAGACATGGTCGGGAAACTGTGGCAATACGGGACATTGTGACA

                                   NcoI
     N  Q  C  K  S  W  E  G  A  A  H  G  A  C  H  V  R  N  G  K
241  ACCAATGTAAATCATGGGAGGGTGCGGCCCATGGAGCGTGTCATGTGCGTAACGGGAAAC

                                             HindIII
     H  M  C  F  C  Y  F  N  C  K  K  A  E  K  L  A  Q  D  K  L
301  ACATGTGTTTCTGTTACTTCAATTGTAAAAAGCCGAAAAGCTTGCTCAAGACAAACTTA
                                             HindIII
     K  A  E  Q  L  A  Q  D  K  L  N  A  Q  K  L  D  R  D  A  K
361  AAGCCGAACAACTCGCTCAAGACAAACTTAATGCCCAAAAGCTTGACCGTGATGCCAAGA

     K  V  V  P  N  V  E  H  P
421  AAGTGGTTCCAAACGTTGAACATCCG
```

Fig.1B.

```
                                                           M  A  K
  1  GTGCCCCGGGTCACGAAGTTCGGCACATCTTAGCGTTATGCATAAGTCAAAAATGGCCAA

      N  S  V  A  F  F  A  L  C  L  L  L  F  I  L  A  I  S  E  I
 61  AAATTCAGTTGCTTTCTTTGCATTGTGCCTGCTTCTTTTCATTCTTGCTATCTCAGAAAT

      R  S  V  K  G  E  L  C  E  K  A  S  K  T  W  S  G  N  C  G
121  CAGATCGGTGAAGGGGGAATTATGTGAGAAGGCAAGCAAGACATGGTCTGGAAATTGTGG

      N  T  R  H  C  D  D  Q  C  K  S  W  E  G  A  A  H  G  A  C
181  CAATACAAGACACTGTGATGACCAGTGCAAGTCTTGGGAGGGTGCAGCCCATGGAGCTTG

      H  V  R  G  G  K  H  M  C  F  C  Y  F  N  C  P  K  A  Q  K
241  TCACGTGCGCGGTGGGAAACACATGTGCTTCTGCTACTTCAACTGTCCCAAAGCCCAGAA

      L  A  E  D  K  L  R  A  A  E  L  A  K  E  K  N  N  I  G  A
301  GTTGGCTGAGGATAAACTCAGAGCAGCAGAGCTAGCAAAGGAGAAGAATAATATTGGAGC

      E  K  V  P  S  A  T  P
361  TGAAAAGGTGCCTTCAGCCACACCTTGAGTACTAACAAA
```

Fig.2A.

```
          M  A  K  N  S  V  A  F  L  A  F  L  L  L  L  F  V
  1 GGCACGAGTAATGGCCAAAAATTCAGTTGCTTTCTTAGCATTTCTTCTGCTTCTTTTCGT

     L  A  I  S  E  I  G  S  V  K  G  E  L  C  E  K  A  S  K  T
 61 TCTTGCTATCTCAGAAATCGGATCGGTGAAGGGGAATTATGTGAGAAGGCAAGCAAGAC

     W  S  G  N  C  G  N  T  R  H  C  D  D  Q  C  K  S  W  E  G
121 ATGGTCTGGAAATTGTGGCAATACAAGACACTGTGATGACCAGTGCAAGTCTTGGGAGGG

     A  A  H  G  A  C  H  V  R  G  G  K  H  M  C  F  C  Y  F  N
181 CGCAGCCCATGGAGCTTGTCACGTGCGCGGTGGGAAACACATGTGCTTTTGCTACTTCAA

     C  S  K  A  Q  K  L  A  Q  D  K  L  K  A  D  K  L  A  K  E
241 CTGTTCCAAAGCCCAGAAGCTGGCTCAGGATAAACTCAAAGCCGACAAGCTCGCCAAGGA

     K  S  E  A  E  K  V  P  A  T  P
301 GAAGAGTGAAGCCGAAAAGGTGCCAGCTACACCTTGAGTACTAACAAGTGTTGTATGATT

361 ATGAATAAAGAGAAAATGCTTTCTAGTTACCATATTTAGCATTCTCTAATGTGTAATGTT

421 TGTTGCTTTTGGAACTAATTGCTTAACTATGATTCCAGCTAATAATGTTTTAAGTATATA

481 ATATAAGTTATCTTATTTTGAAGCCTGTAAAAAAAAAAAAAAA
```

Fig.2B.

```
                                      M  A  K  N  S  V  A  F  F  A  F  V
  1  CGGCACGAGGCACAATCTCAAAAATGGCCAAAAATTCGGTTGCTTTCTTTGCATTTGTCC

     L  L  L  F  V  L  A  I  S  E  I  G  S  V  K  G  E  L  C  E
 61  TGCTTCTTTTCGTTCTTGCTATCTCAGAAATTGGATCGGTGAAGGGAGAATTATGTGAGA

     K  A  S  K  T  W  S  G  N  C  G  I  T  S  H  C  D  N  Q  C
121  AGGCAAGCAAGACATGGTCTGGAAATTGTGGCATCACATCACACTGTGACAACCAGTGCC

     R  S  W  E  G  A  I  H  G  A  C  H  V  R  G  G  K  H  M  C
181  GGTCGTGGGAGGGTGCAATCCATGGAGCTTGTCACGTGCGCGGTGGGAAACACATGTGCT

     F  C  Y  F  N  C  S  K  A  D  E  L  A  K  E  K  I  E  A  E
241  TCTGCTACTTCAACTGTTCCAAAGCCGATGAGCTCGCGAAGGAGAAGATTGAAGCCGAAA

     K  M  P  A  T  P
301  AGATGCCAGCCACACCTTGAGTACTAACAAATGCTATATGATTATAAATAAAGAGAAAAT

361  GCTTTCTAAAAAAAAAAAAAAAAAA
```

Fig.3.

```
                               M  V  N  R  S  V  A  F  S  V  F  V  L  I
  1   GGCACGAGCCTATTAAAAAATGGTGAATCGATCGGTTGCTTTCTCCGTGTTCGTTCTGAT
        L  F  V  L  A  I  S  D  I  T  S  V  R  G  E  V  C  E  K  A
 61   CCTTTTCGTGCTCGCCATCTCAGATATCACAAGTGTGAGAGGAGAAGTATGCGAGAAAGC
        S  K  T  W  S  G  N  C  G  N  T  G  H  C  D  N  Q  C  K  Y
121   TAGCAAGACATGGTCAGGAAACTGTGGCAACACGGGACACTGTGACAACCAATGTAAATA
        W  E  G  A  A  H  G  A  C  H  V  R  G  G  K  H  M  C  F  C
181   CTGGGAGGGGGCGGCCCATGGGGCGTGCCACGTGCGTGGAGGGAAACACATGTGTTTCTG
        Y  F  K  C  P  K  A  E  K  L  A  Q  D  K  V  N  A  Q  E  L
241   CTACTTCAAGTGTCCCAAAGCCGAAAAGCTTGCTCAAGACAAAGTTAATGCCCAAGAGCT
        D  R  D  A  K  K  V  I  P  N  V  E  H  P
301   TGACCGTGATGCCAAGAAAGTGATTCCGAACGTTGAACATCCGTGAAAGGGTCGGTTTCT
361   TTAAATAGAAAGTCTTAGATTACGAATGCGAATAACTATAGAAAATGTTTGCTAAATGTC
421   ACATTATAATTAGAACTTTATGATTGTTGTCAATAGGGCATTTTCTTGTTAGTGATATGT
481   GTAATAAGGTGATGCTTTTATGCTTTTCGTGCGTAAGAGTTTTCGACTATGTGTAATAAA
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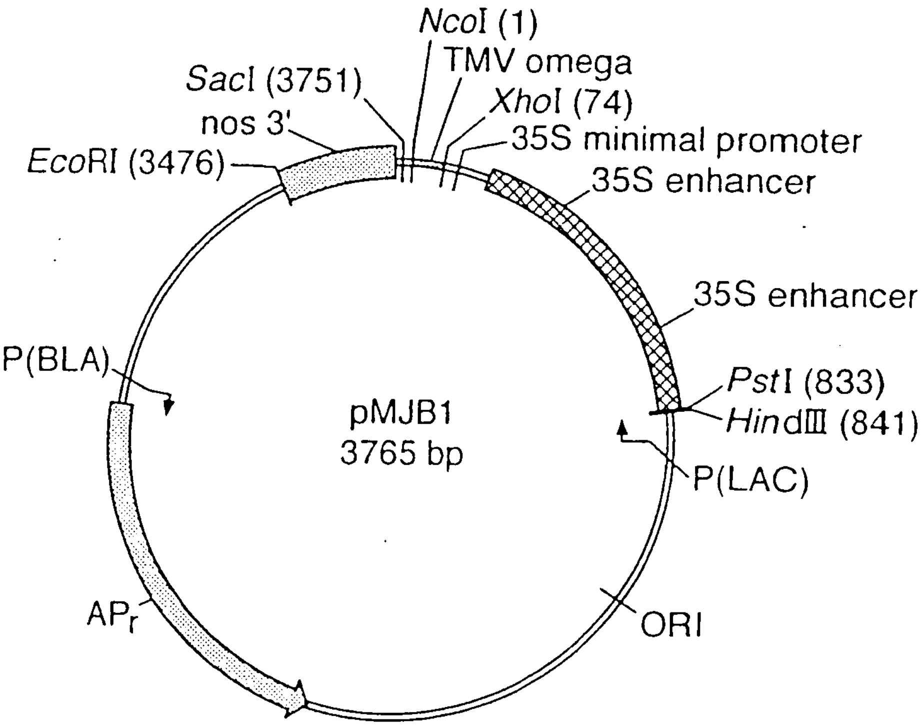
Fig.4.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TMV omega
XhoI (74)
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35S enhancer
SacI (3751)
nos 3'
EcoRI (3476)
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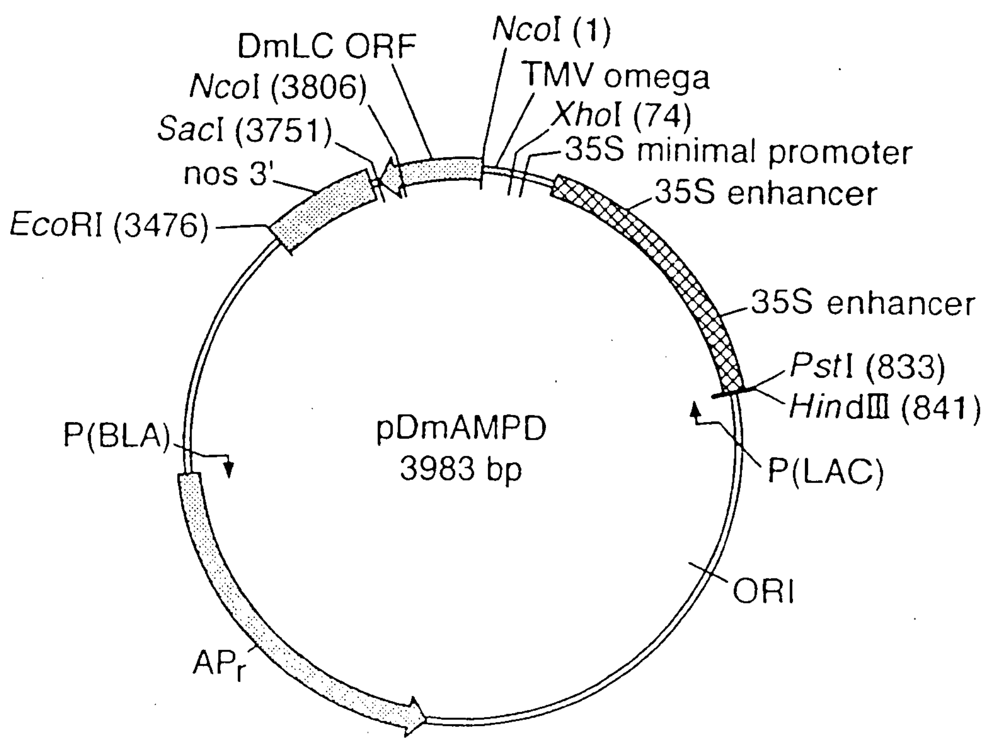
PstI (833)
HindIII (841)
P(BLA)
pMJB1
3765 bp
P(LAC)
APr
ORI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TMV omega
NcoI (3806)
XhoI (74)
SacI (3751)
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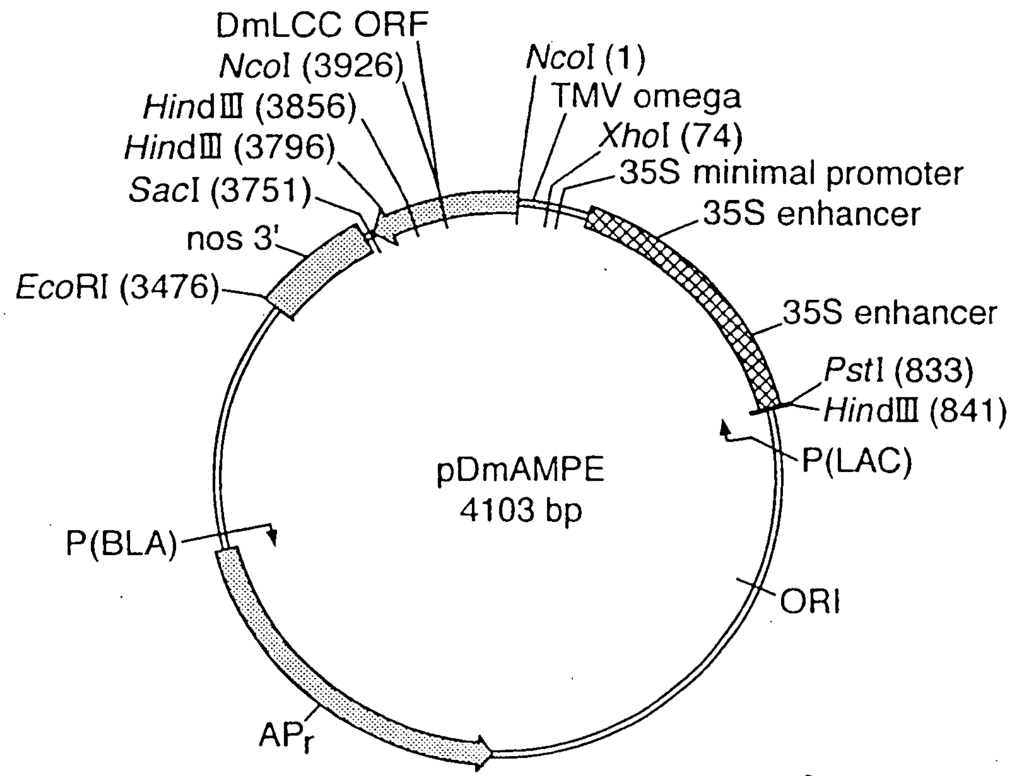
nos 3'
35S enhancer
EcoRI (3476)
35S enhancer
PstI (833)
HindIII (841)
P(BLA)
pDmAMPD
3983 bp
P(LAC)
ORI
APr

Fig.4 (Cont).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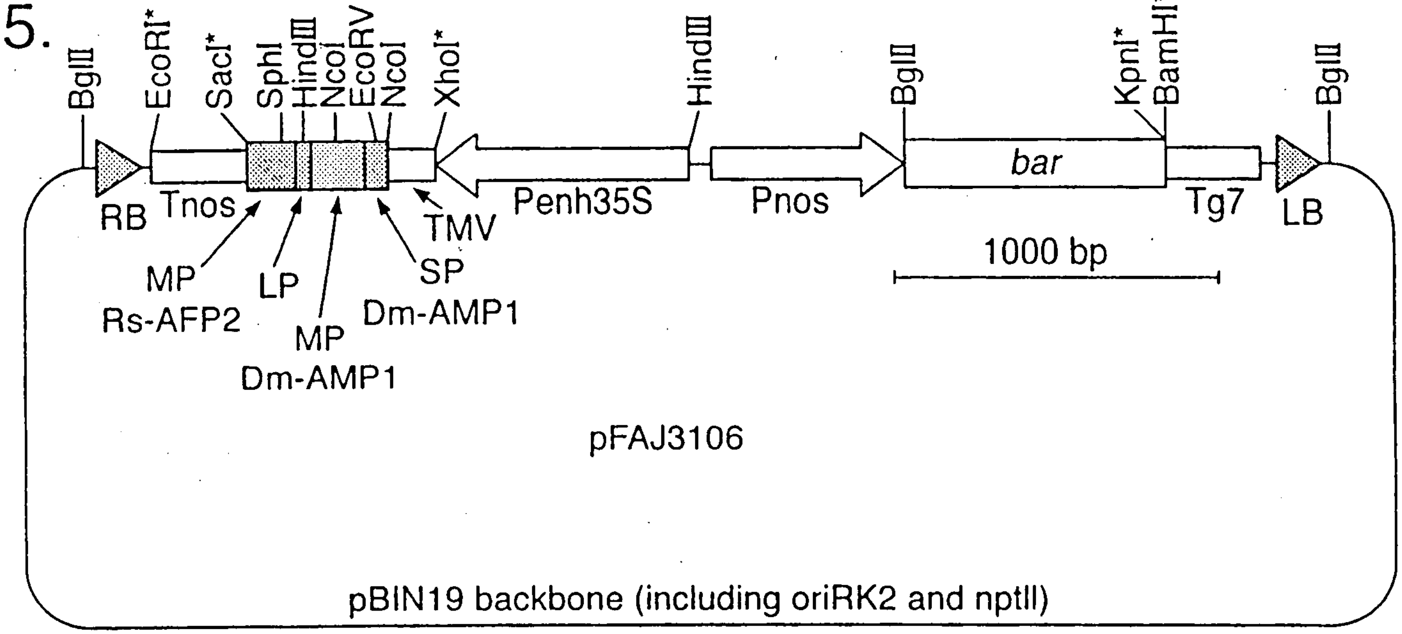
HindIII (3796)
SacI (3751)
nos 3'
EcoRI (3476)
NcoI (1)
TMV omega
XhoI (74)
35S minimal promoter
35S enhancer
35S enhancer
PstI (833)
HindIII (841)
P(LAC)
pDmAMPE
4103 bp
P(BLA)
ORI
APr

Fig.5.

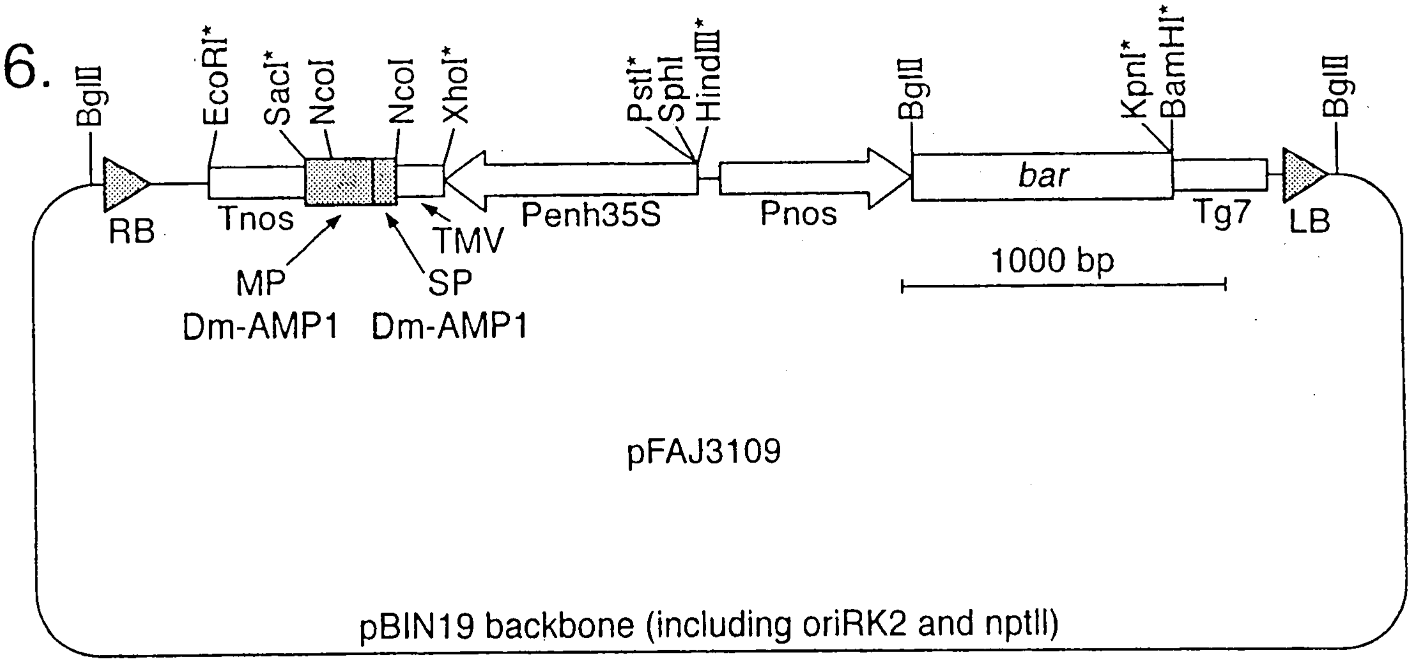


Symbols

RB: right border of T-DNA
Tnos: terminator of T-DNA nopaline synthase gene
MP Rs-AFP2: mature protein domain of Rs-AFP2
LP: first 16 AA of Dm-AMP1 C-terminal propeptide and subtilisin-like protease recognition site IGKR
MP Dm-AMP1: mature protein domain of Dm-AMP1 cDNA
SP Dm-AMP1: signal peptide domain of Dm-AMP1 cDNA
TMV: tobacco mosaic virus 5' leader sequence
Penh35S: promotor of 35S RNA of cauliflower mosaic virus with duplicated enhancer region
Pnos: promotor of T-DNA nopaline synthase gene
bar: basta resistance encoding gene
Tg7: terminator of T-DNA gene 7
LB: left border of T-DNA

*: unique restriction site

Fig.6.



Symbols

RB: right border of T-DNA
Tnos: terminator of T-DNA nopaline synthase gene
MP Dm-AMP1: mature protein domain of Dm-AMP1
SP Dm-AMP1: signal peptide domain of Dm-AMP1 cDNA
TMV: tobacco mosaic virus 5' leader sequence
Penh35S: promotor of 35S RNA of cauliflower mosaic virus with duplicated enhancer region
Pnos: promotor of T-DNA nopaline synthase gene
bar: basta resistance encoding gene
Tg7: terminator of T-DNA gene 7
LB: left border of T-DNA

*: unique restriction site

Fig.7. pFAJ3106

XhoI
CTCGAGTATTTTTACAACAATTACCAACAACAACAAACAACAAACAACATTACAATTACT

NcoI
ATTTACAATTACACCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCGTTCTGATCCTT
M V N R S V A F S A F V L I L

TTCGTGCTCGCCATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGC
F V L A I S D I A S V S G E L C E K A S

AAGACGTGGTCGGGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGG
K T W S G N C G N T G H C D N Q C K S W

GAGGGTGCGGCCCATGGAGCGTGTCATGTGCGTAACGGGAAACACATGTGTTTCTGTTAC
E G A A H G A C H V R N G K H M C F C Y

TTCAATTGTAAAAAAGCCGAAAAGCTTGCTCAAGACAAACTTAAAGCCGAACAACTCATC
F N C K K A E K L A Q D K L K A E Q L I

GGAAAGAGGCAGAAGTTGTGCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAAC
G K R Q K L C Q R P S G T W S G V C G N

AATAACGCATGCAAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGGATCTTGCAAC
N N A C K N Q C I R L E K A R H G S C N

SacI
TATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGTTAATAGGAGCTC
Y V F P A H K C I C Y F P C - -

Fig.8.

pFAJ3109

XhoI
CTCGAGTATTTTTACAACAATTACCAACAACAACAAACAACAAACAACATTACAATTACT

NcoI
ATTTACAATTACACCATGGTGAATCGGTCGGTTGCGTTCTCCGCGTTCGTTCTGATCCTT
M V N R S V A F S A F V L I L

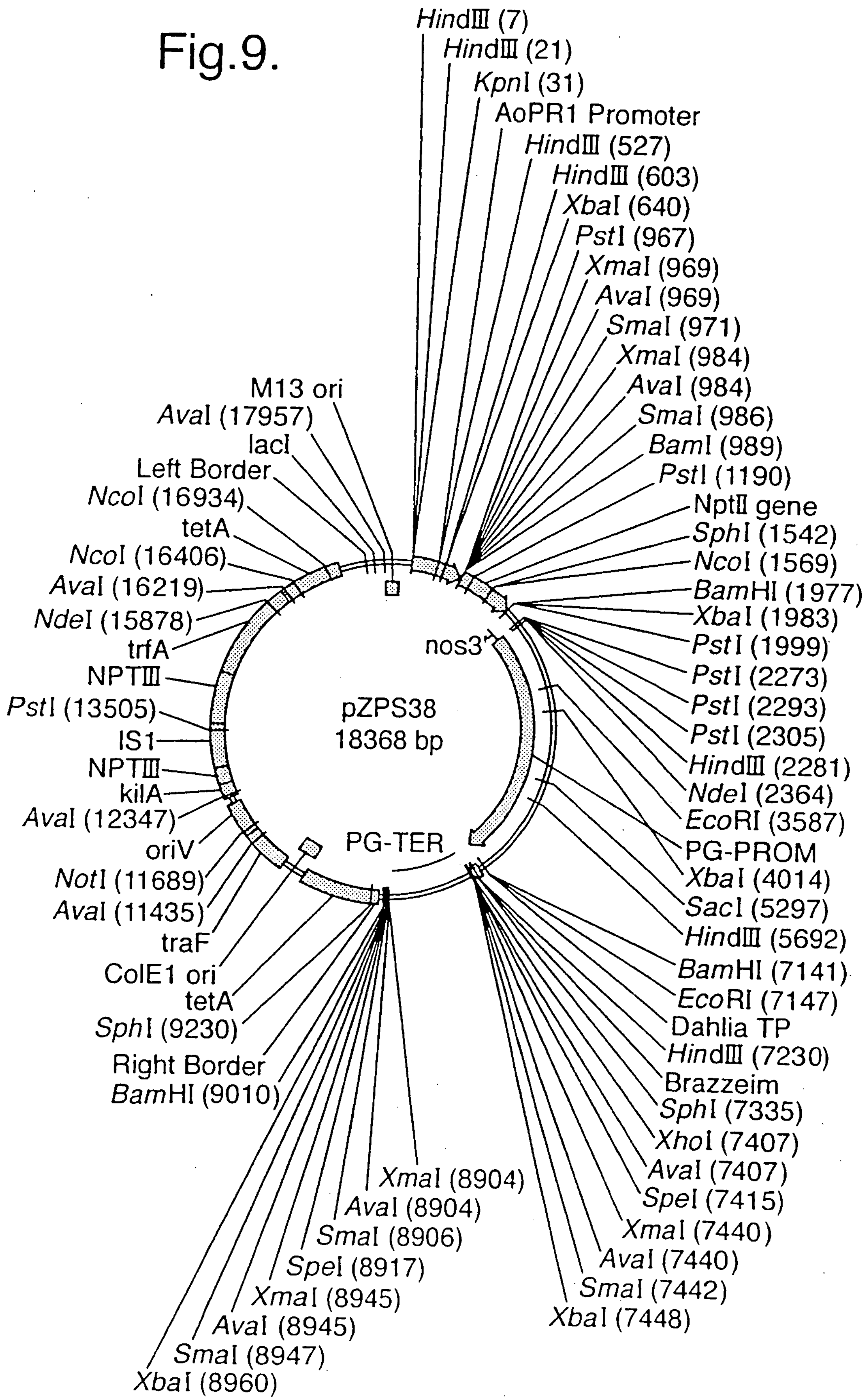
TTCGTGCTCGCCATCTCAGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGC
F V L A I S D I A S V S G E L C E K A S

AAGACGTGGTCGGGCAACTGTGGCAACACGGGACATTGTGACAACCAATGTAAATCATGG
K T W S G N C G N T G H C D N Q C K S W

GAGGGTGCGGCCCATGGAGCGTGTCATGTGCGTAATGGGAAACACATGTGTTTCTGTTAC
E G A A H G A C H V R N G K H M C F C Y

SacI
TTCAATTGTTGAGCTC
F N C -

Fig.9.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KpnI (31)
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XbaI (640)
PstI (967)
XmaI (969)
AvaI (969)
SmaI (971)
XmaI (984)
AvaI (984)
SmaI (986)
BamI (989)
PstI (1190)
NptII gene
SphI (1542)
NcoI (1569)
BamHI (1977)
XbaI (1983)
PstI (1999)
PstI (2273)
PstI (2293)
PstI (2305)
HindIII (2281)
NdeI (2364)
EcoRI (3587)
PG-PROM
XbaI (4014)
SacI (5297)
HindIII (5692)
BamHI (7141)
EcoRI (7147)
Dahlia TP
HindIII (7230)
Brazzeim
SphI (7335)
XhoI (7407)
AvaI (7407)
SpeI (7415)
XmaI (7440)
AvaI (7440)
SmaI (7442)
XbaI (7448)
XmaI (8904)
AvaI (8904)
SmaI (8906)
SpeI (8917)
XmaI (8945)
AvaI (8945)
SmaI (8947)
XbaI (8960)
BamHI (9010)
Right Border
SphI (9230)
tetA
ColE1 ori
traF
AvaI (11435)
NotI (11689)
oriV
AvaI (12347)
kilA
NPTIII
IS1
PstI (13505)
NPTIII
trfA
NdeI (15878)
AvaI (16219)
NcoI (16406)
tetA
NcoI (16934)
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lacI
AvaI (17957)
M13 ori
nos3'
pZPS38
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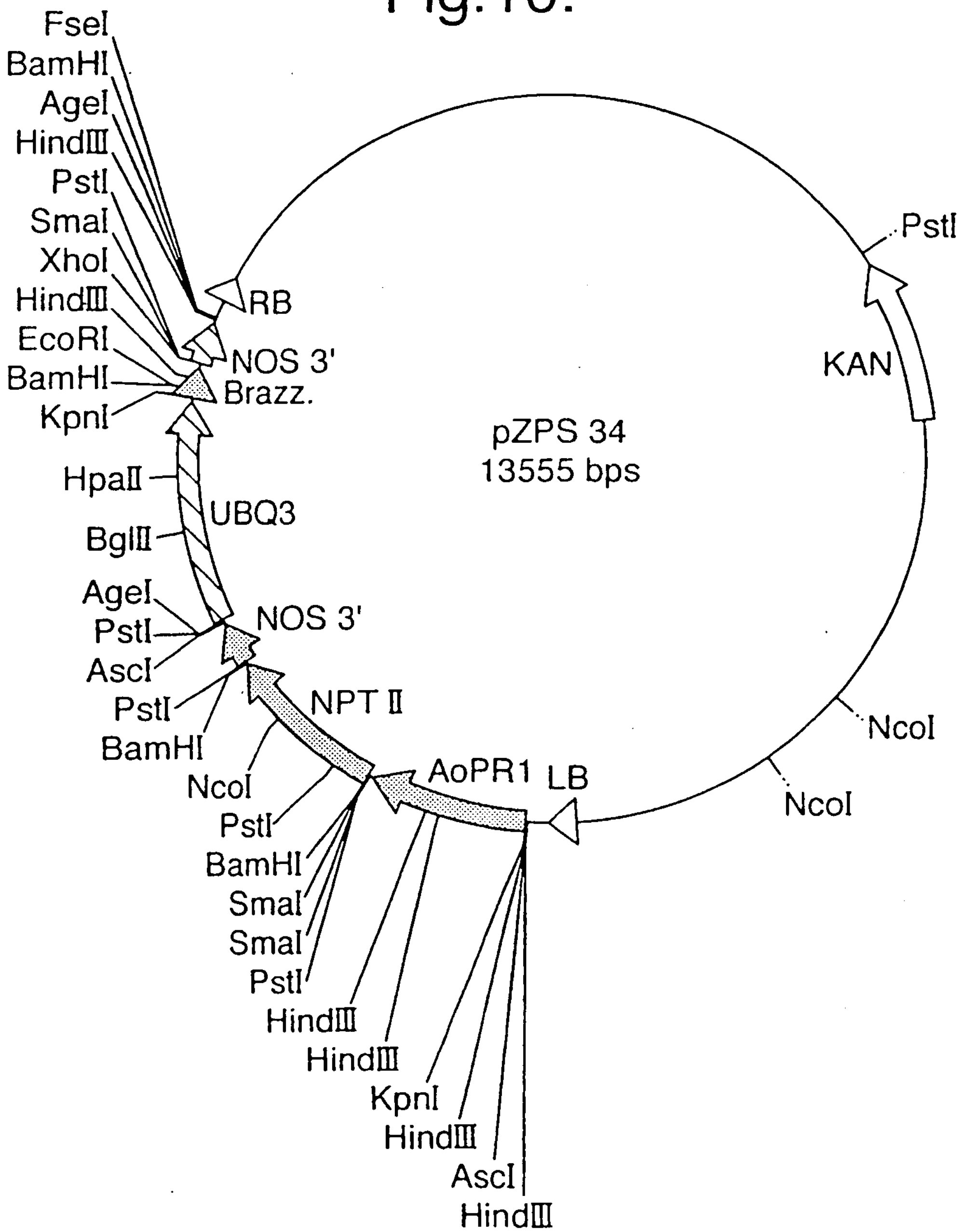
PG-TER

Fig.10.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AgeI
HindIII
PstI
SmaI
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KpnI
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Brazz.
HpaII
UBQ3
BglII
AgeI
PstI
AscI
NOS 3'
PstI
BamHI
NPT II
NcoI
PstI
BamHI
SmaI
SmaI
PstI
HindIII
HindIII
KpnI
HindIII
AscI
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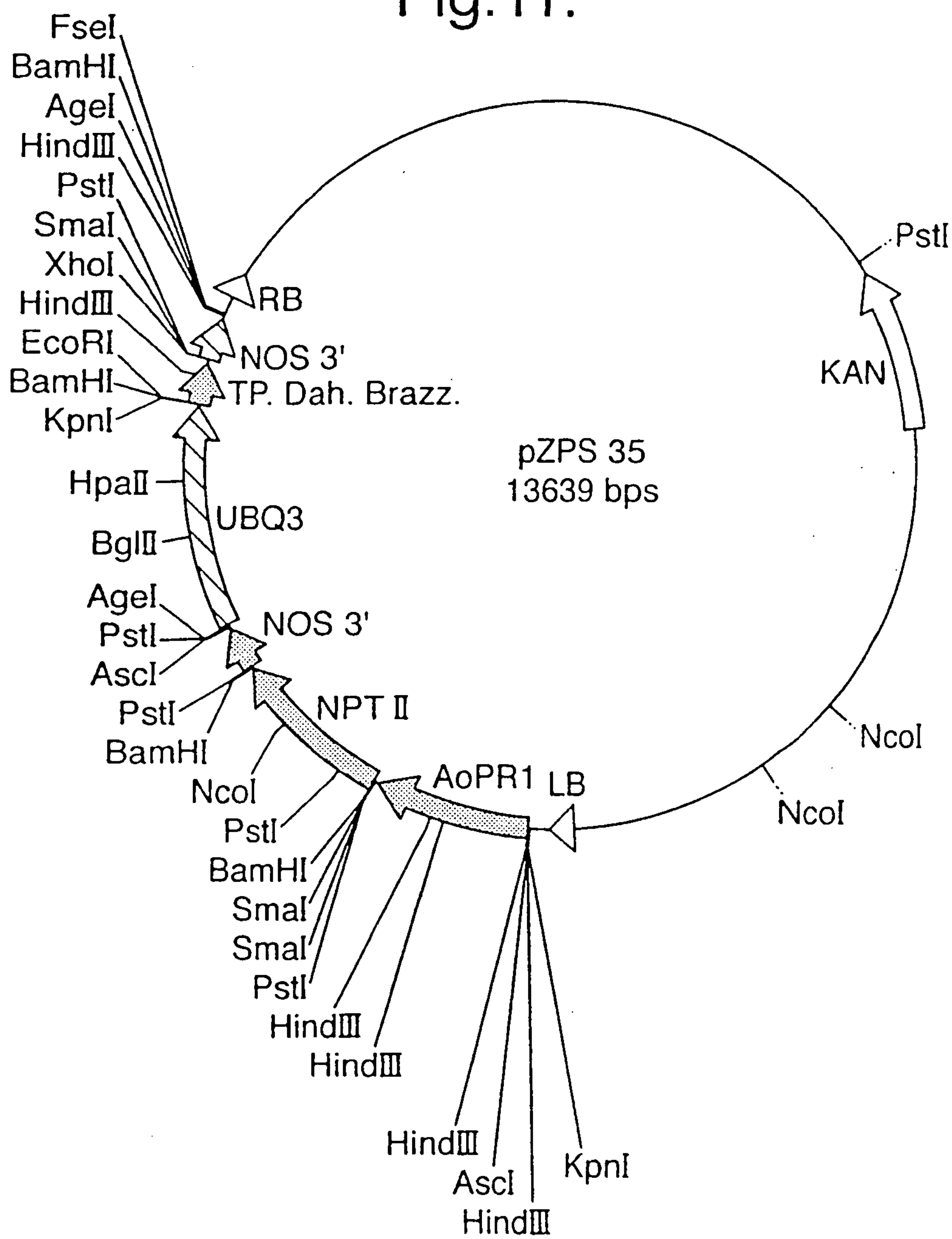
AoPR1
LB
NcoI
NcoI
KAN
PstI
pZPS 34
13555 bps

Fig.11.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RB
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TP. Dah. Brazz.
HpaII
UBQ3
BglII
AgeI
PstI
AscI
NOS 3'
PstI
BamHI
NPT II
NcoI
PstI
BamHI
SmaI
SmaI
PstI
HindIII
HindIII
AoPR1
LB
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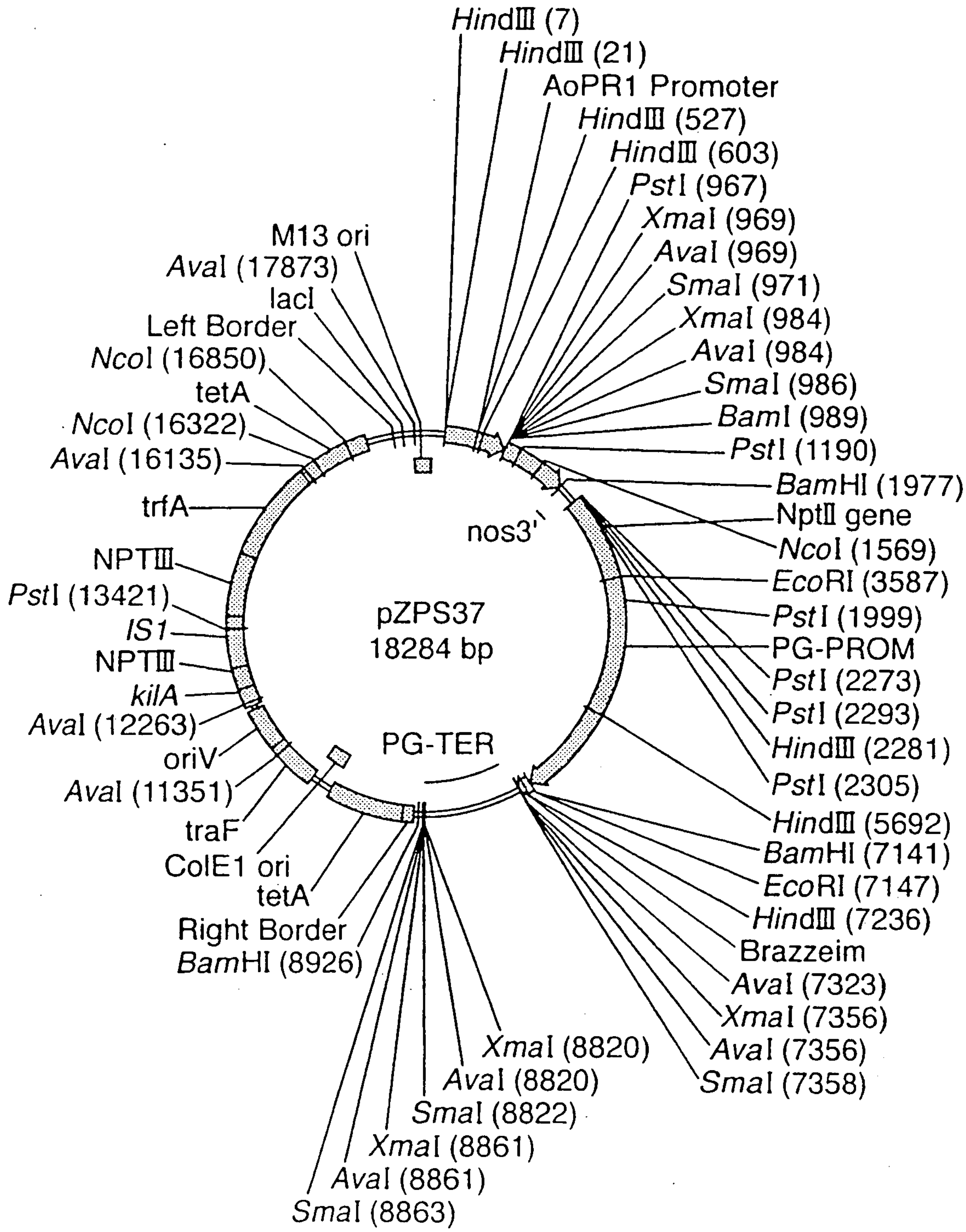
13639 bps

Fig.12.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PG-PROM
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BamHI (7141)
EcoRI (7147)
HindIII (7236)
Brazzeim
AvaI (7323)
XmaI (7356)
AvaI (7356)
SmaI (7358)
XmaI (8820)
AvaI (8820)
SmaI (8822)
XmaI (8861)
AvaI (8861)
SmaI (8863)
BamHI (8926)
Right Border
tetA
ColE1 ori
traF
AvaI (11351)
oriV
AvaI (12263)
kilA
NPTIII
IS1
PstI (13421)
NPTIII
trfA
AvaI (16135)
NcoI (16322)
tetA
NcoI (16850)
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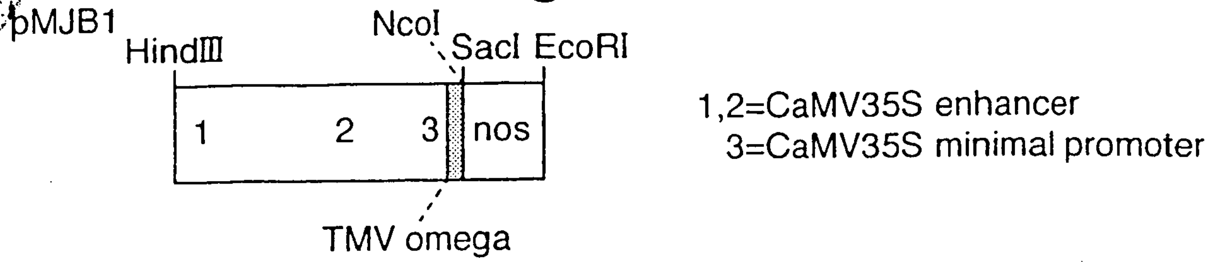
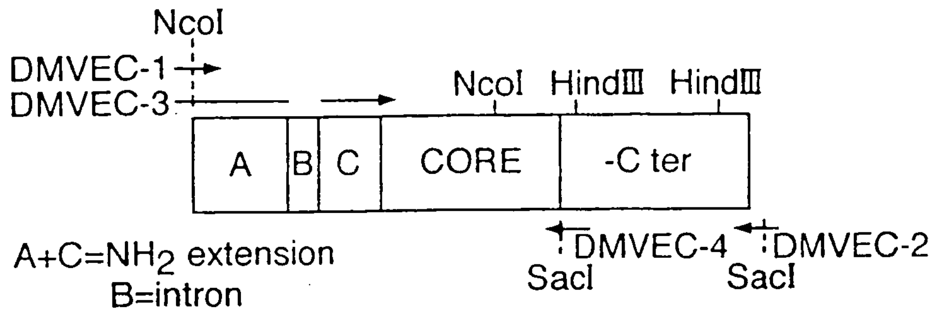
lacI
AvaI (17873)
M13 ori
nos3'
pZPS37
18284 bp
PG-TER

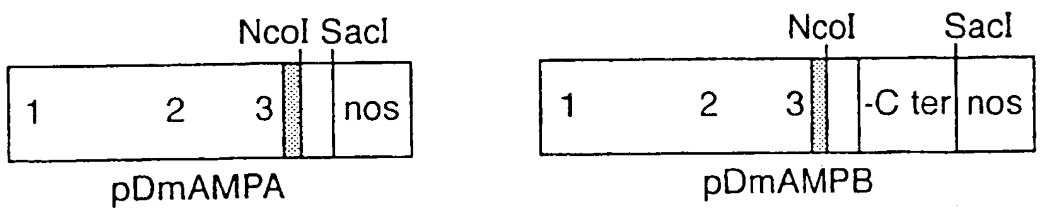
Fig.13.



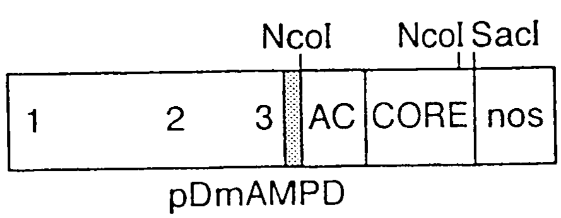
Structure of DmAMP1 Gene and position of vector construction oligonucleotides



PCR Dahlia genomic DNA with DMVEC-1 and DMVEC-2, isolate 450 bp product.
PCR 450 bp DMVEC-1/DMVEC-2 PCR product with DMVEC 1 and 4.
Isolate 60 bp NcoI / SacI fragment, clone into pMJB1 NcoI / SacI=pDmAMPA.
Cut 450 bp DMVEC-1/DMVEC-2 PCR product NcoI / SacI . Isolate 180 bp NcoI / SacI fragment, clone into pMJB1 NcoI / SacI =pDmAMPB



PCR 450 bp DMVEC-1/DMVEC-2 PCR product with DMVEC 3 and 4.
Isolate 150 bp NcoI fragment, clone into pDmAMPA and pDmAMPB NcoI =pDmAMPD and pDmAMPE



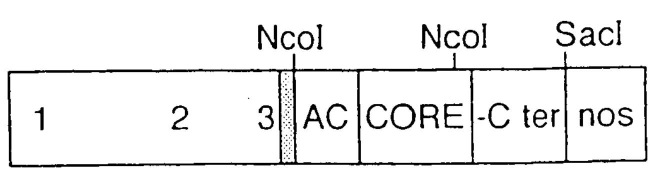


Fig.14.

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		TGG GAG GGA GCT GCT CAT GGA GCT TGC CAT GTT AGA AAC
Sequence ID No.7	Dm-AMP2	GAG GTT TGC GAG AAG GCT TCT AAG ACT TGG TCT GGA AAC

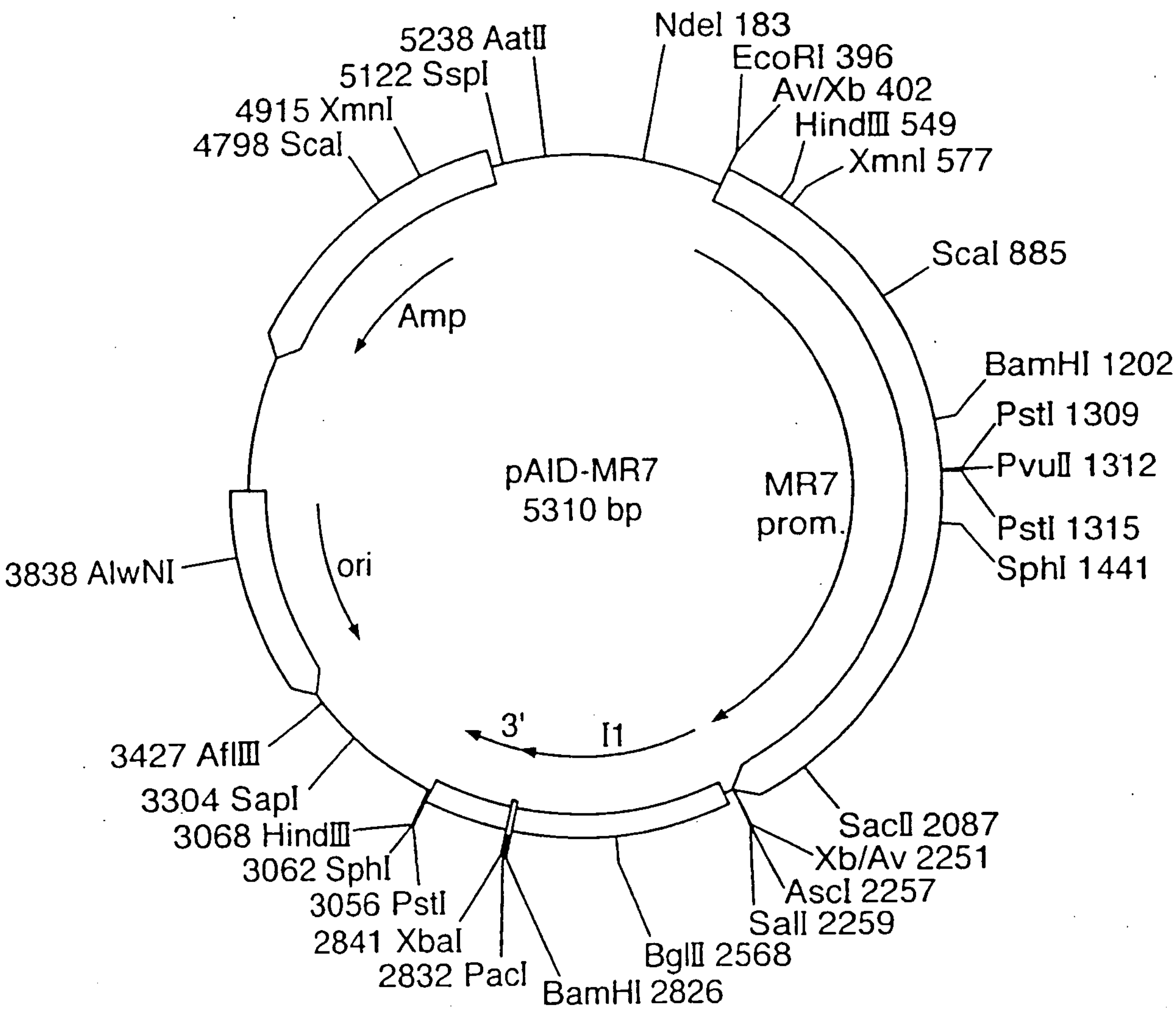
Fig.14 (Cont).

TGC GGA AAC ACT GGA CAT TGC GAT AAC CAA TGC AAG TCT

GGA AAG CAT ATG TGC TTC TGC TAC TTC AAC TGC

TGC GGA AAC ACT GGA CAT TGC ... ...

Fig.15.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NdeI 183
EcoRI 396
5122 SspI
Av/Xb 402
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HindIII 549
4798 ScaI
XmnI 577
ScaI 885
Amp
BamHI 1202
PstI 1309
pAID-MR7
5310 bp
MR7
prom.
PvuII 1312
PstI 1315
SphI 1441
3838 AlwNI
ori
3'
I1
3427 AflIII
3304 SapI
SacII 2087
3068 HindIII
Xb/Av 2251
3062 SphI
AscI 2257
3056 PstI
SalI 2259
2841 XbaI
BglII 2568
2832 PacI
BamHI 2826